

FIG. 1A

CATGGACCCAGATGAACTCCCATTTGGATGAACATTGTGAACGACTGCCTTATGA
 TGCCACCAAATGGGAATTTCCCAGAGACCGCTGAAGCTAGGTAAGCCTCTTG
 GCCGTGGTGCCTTTGGCCAAGTGATTGAAGCAGATGCCTTTGGAATTGACAAG
 ACAGCAACTTGCAGGACAGTAGCAGTCAAAATGTTGAAAGAAGGAGCAACACA
 CAGTGACCATCGAGCTCTCATGTCTGAACTCAAGATCCTCATTCATATTGGTCA
 CCATCTCAATGTGGTCAACCTTCTAGGTGCCTGTACCAAGCCAGGAGGGCCAC
 TCATGGTGATTGTGGAATTTGCAAATTTGGAACCTGTCCACTTACCTGAGGA
 GCAAGAGAAATGAATTTGTCCCCTACAAGACCAAAGGGGCACGATTCCGTCAA
 GGGAAAGACTACGTTGGAGCAATCCCTGTGGATCTGAAACGGCGCTTGGACAG
 CATCACCAGTAGCCAGAGCTCAGCCAGCTCTGGATTGTGGAGGAGAAGTCCC
 TCAGTGATGTAGAAGAAGAGGAAGCTCCTGAAGATCTGTATAAGGACTTCTGT
 ACCTTGGAGCATCTCATCTGTTACAGCTTCCAAGTGGCTAAGGGCATGGAGTTT
 TTGGCATCGGAAAGTGATCCACAGGGACCTGGCGGCACGAAATATCCTCTT
 ATCGGAGAAGAAGCTGGTTAAAATCTGTGACTTTGGCTTGGCCCGGATATTTA
 TAAAGATCCAGATTATGTCAGAAAAGGAGATGCTCGCCTCCCTTTGAAATGGAT
 GGCCCCAGAAACAATTTTGGACAGAGTGACACAATCCAGAGTGACGTCTGGT
 CTTTGGTGTTTTGCTGTGGGAAATATTTCTTAGGTGCTTCTCCATATCCTGG
 GGTAAACATTGATGAAGAATTTGTAGGCGATTGAAAGAAGGAACTAGAATGA
 GGGCCCTGATTATACTACACCAGAAATGTACCAGACCATGCTGGACTGCTGG
 CACGGGGAGCCCAGTCAGAGACCCACGTTTTACAGATTGGTGGAAACATTTGGG
 AAATCTCTTGAAGCTAATGCTCAGCAGGATGGCAAAGACTACATTGTTCTTCC
 GATATCAGAGACTTTGAGCATGGAAGAGGATTCTGGACTCTCTGCTACCTC
 ACCTGTTTCTGTATGGAGGAGGAGGAAGTATGTGACCCCAAATTCATTATGA
 CAACACAGCAGGAATCAGTCAGTATCTGCAGAACAGTAAGCGAAAGAGCCGGC
 CTGTGAGTGTAACAAATTTGAAGATATCCCGTTAGAAGAACCAGAAGTAAAG
 TAATCCCAGATGACAACCAGACGACAGTGGTATGGTTCTTGCCTCAGAAGAG
 CTGAAAACCTTTGGAAGACAGAACCAATTATCTCCATCTTTTGGTGGAAATGGT
 CCCAGCAAAGCAGGGAGTCTGTGCCATCTGAAGGCTCAAACCAGACAAGCG
 GCTACCAGTCCGATATCACTCCGATGACACAGACACCACCGTACTCCAGT
 GAGGAAGCAGAACTTTTAAAGCTGATAGAGATTGGAGTGCAACCGGTAGCAC
 AGCCCAGATTCTCCAGCCTGACTCGGGACCACACTGAGCTCTCCTCCTGTTTA
 A (SEQ ID NO:1)

FIG. 1B

MESKVL LAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILT IKANTTLQTTTCRGQR
 DLDWLWPNNQSGSEQRVEVTECSGLFCKLTIPKVI GNDTGAYKCFYRETDLAS
 VIYVYVQDYRSPFIASVSDQHGVVYI IENKNKTVVIPCLGSI SNLNVSLCARYPEKR
 FVPDGNRI SWDSKKGFI IPSYMI SYAGMVFEAKINDESYQSIMYI VVVVGYRIYDV
 VLSPSHGIELSVGEKLVLNCTARTELVNGIDFNMEYPSKHKHKL VNRDLKTQS
 GSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFSGSM
 ESLVEATVGERVRIPAKYLGYPPEIKWYKNGIPLESNHTIKAGHVLTIMEVSEDT
 GNYTVILTNPISKEKQSHVSLVYVPPQIGEKSLISPVDYQYGTQTLTCTVYAI P
 PPHIHWWQLEEECANEPSQAVSVTNYPCEEWRSEDFQCGNKIEVNKNQFA
 LIEGKNKTVSTLVQAANVSALYKCEAVNKVGRGERVISFHVTRGPETTLQPMQ
 TEQESVSLWCTADRSTFENLTWYKLGQPLPIHVGE LPTPVCKNLDTLWKL NATM
 FSNSTNDILIMELKNASLQDQD TVCLAQDRKTKKRHCVRQLTVLERVAPTTGN
 LENQTTSIGESI EVSCTASGNPPQIMWFKDNETLVEDSGIVLKDGNRNLTI RRVK
 EDEGLYTCQACSVLGCAKVEAFFIEGAQKTNLEIIILVGTAVIAMFFWLLVILRT
 VKRANGGELKTGYLSIVMDPDELPLDEH CERLPYDASKWEFPRDRLKLGKPLGRG
 AFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNV
 NLLGACTKPGGPLMVI VEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGDYVG
 AIPVDLKRRLDSITSSQSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQ
 VAKGMEFLASRKC IHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDAR
 LPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEFCRRLKEGT
 RMRAPDYTTPEMYQTMLDCWHGEPSQRPTFFSELVEHLGNLLQANAQQDGKDYIVL
 PISETLSMEEDSGLSLPTSPVSCMEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVS
 VKTFEDIPLEEPEVKVIPPDDNQD SGMLASEELKTLEDRTKLSPSFGGMVPSKSRE
 SVASEGSNQTSGYQSGYHSDDTDTTVYSSEEAE LKLIEIGVQTGSTAQI LQPDSGT
 TLSSPPV (SEQ ID NO:2)

FIG.2

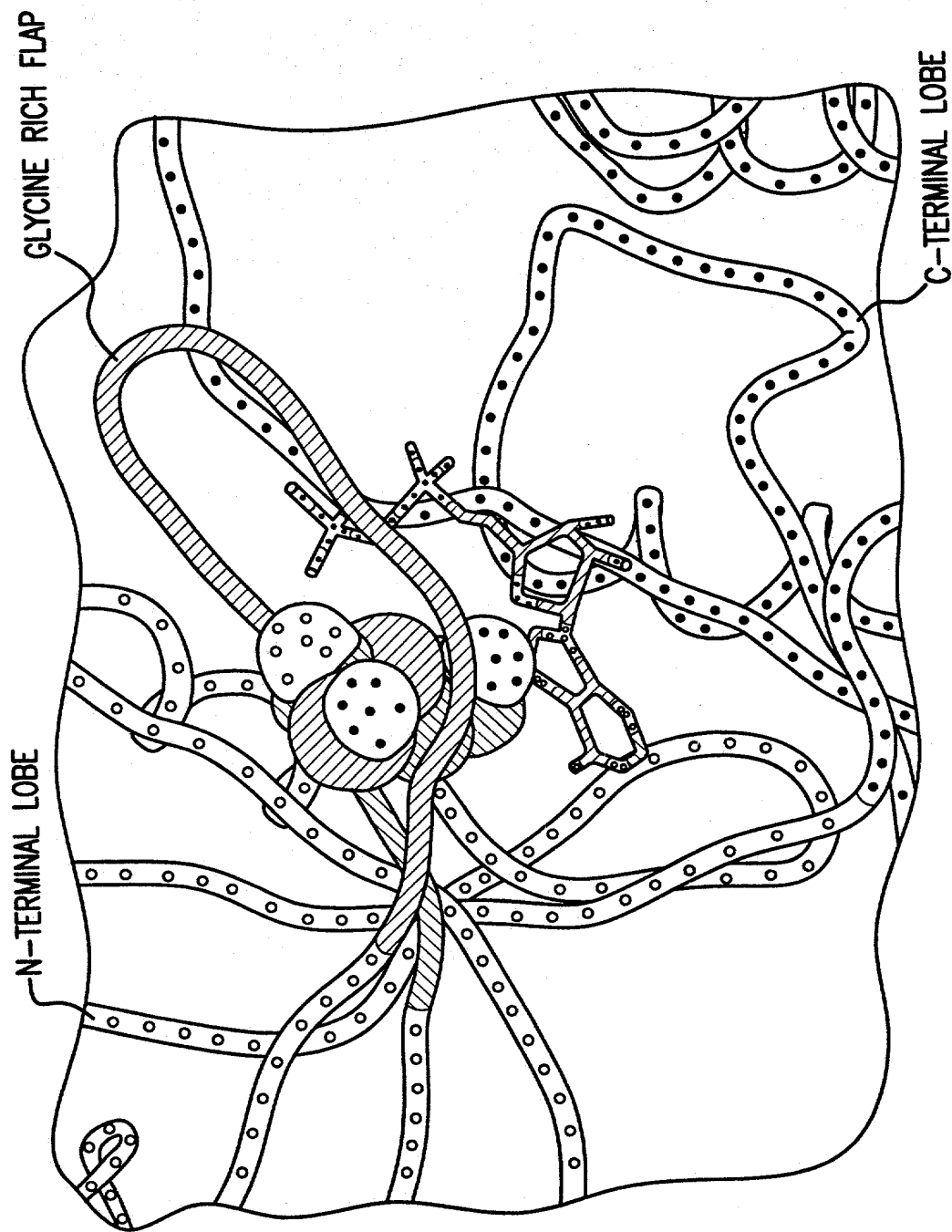


FIG.3A

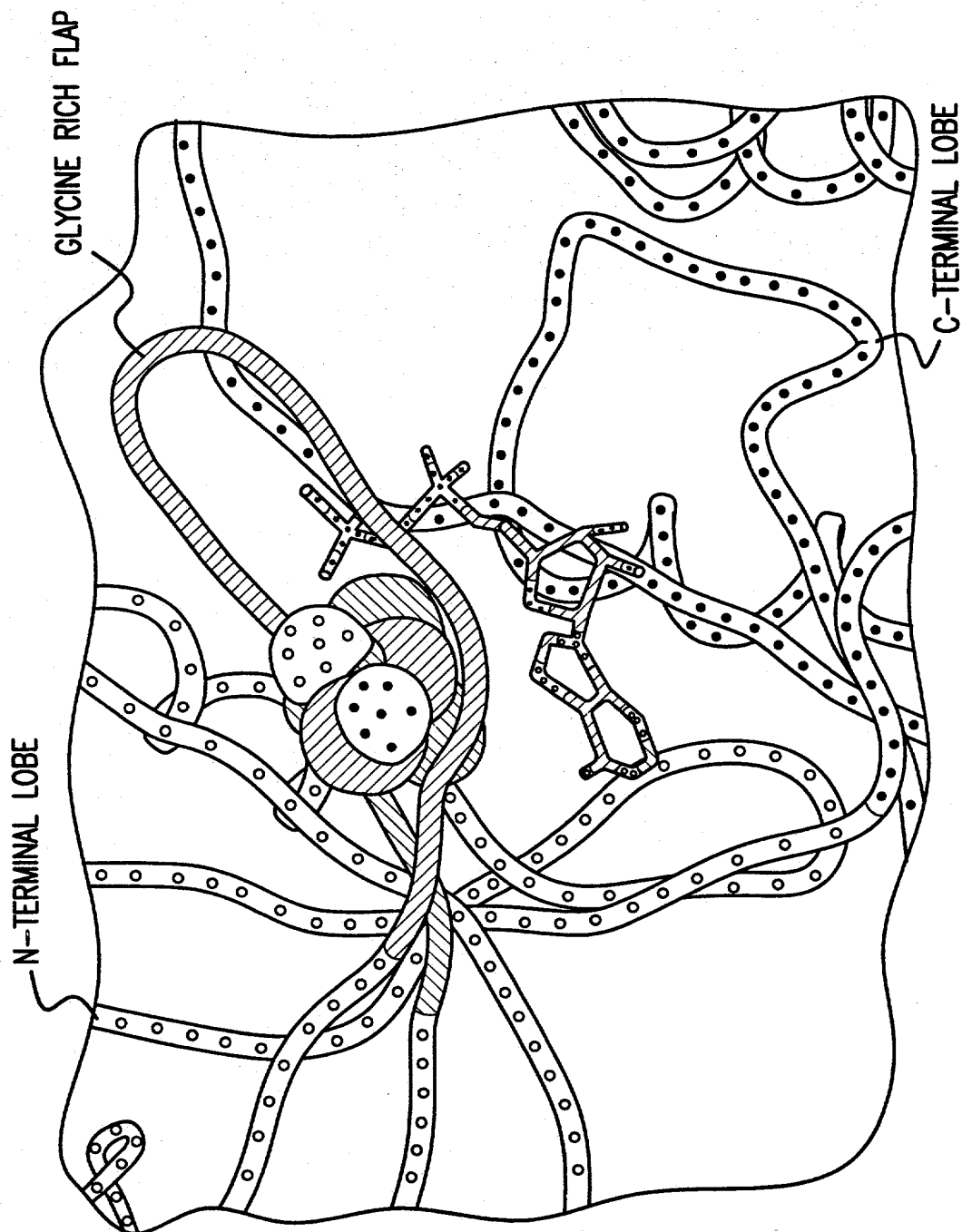


FIG.3B

Anti-phosphotyrosine

E848			V848	
12	12	120	12	12
-	+	+	-	+



FIG.4A

Anti-KDR

E848	V848
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120	12	Enzyme (ng)
-	-	ATP (1 mM)

kDa

— 121



— 78

FIG.4B